

Fig. 1

1	ATG	GCT	GGA	CCT	GCC	ACC	CAG	AGC	CCC	ATG	AAG	CTG	ATG	GCC	CTG	45
46	CAG	CTG	CTG	CTG	TGG	AGT	GCA	CTC	TGG	ACA	GTG	CAG	GAA	GCC	ACC	90
91	CCC	CTG	GGC	CCT	GCC	AGC	TCC	CTG	CCC	CAG	AGC	TTC	CTG	CTC	AAG	135
136	TGC	TTA	GAG	CAA	GTG	AGG	AAG	ATC	CAG	GGC	GAT	GGC	GCA	GCG	CTC	180
181	CAG	GAG	AAG	CTG	GCA	GGC	TGC	TTG	AGC	CAA	CTC	CAT	AGC	GGC	CTT	225
226	TTC	CTC	TAC	CAG	GGG	CTC	CTG	CAG	GCC	CTG	GAA	GGG	ATC	TCC	CCC	270
271	GAG	TTG	GGT	CCC	ACC	TTG	GAC	ACA	CTG	CAG	CTG	GAC	GTC	GCC	GAC	315
316	TTT	GCC	ACC	ACC	ATC	TGG	CAG	CAG	ATG	GAA	GAA	CTG	GGA	ATG	GCC	360
361	CCT	GCC	CTG	CAG	CCC	ACC	CAG	GGT	GCC	ATG	CCG	GCC	TTC	GCC	TCT	405
406	GCT	TTC	CAG	CGC	CGG	GCA	GGA	GGG	GTC	CTA	GTT	GCC	TCC	CAT	CTG	450
451	CAG	AGC	TTC	CTG	GAG	GTG	TCG	TAC	CGC	GTT	CTA	CGC	CAC	CTT	GCC	495
496	CAG	CCC	TAA	TAA												508

stop codon (see: SEQ ID NO: 17)

Fig. 2

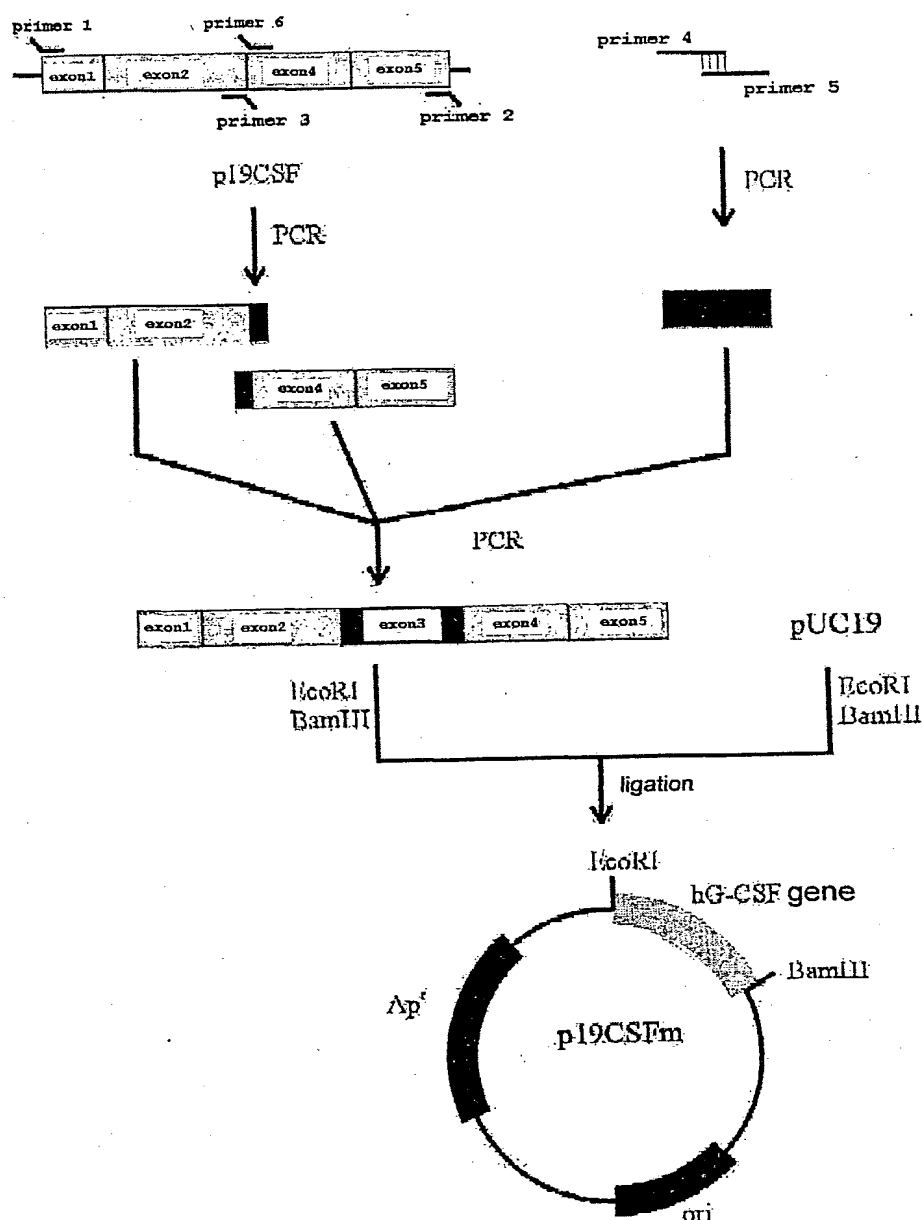


Fig. 3

⁻³⁰
 1 ATG GCT GGA CCT GCC ACC CAG AGC CCC ATG AAG CTG ATG GCC CTG ⁻¹⁶ 45
⁻¹⁵
 46 CAG CTG CTG CTG TGG AGT GCA CTC TGG ACA GTG CAG GAA GCC ⁻¹ ⁺¹ ACC 90
 Thr
²
 91 CCC CTG GGC CCT GCC AGC TCC CTG CCC CAG AGC TTC CTG CTC AAG ¹⁶ 135
 Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
¹⁷
 136 TGC TTA GAG CAA GTG AGG AAG ATC CAG GGC GAT GGC GCA GCG CTC ³¹ 180
 Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
³²
 181 CAG GAG AAG CTG TGT GCC ACC TAC AAG CTG TGC CAC CCC GAG GAG ⁴⁶ 225
 Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
⁴⁷
 226 CTG GTG CTG CTC GGA CAC TCT CTG GGC ATC CCC TGG GCT GCC CTG ⁶¹ 270
 Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu
⁶²
 271 AGC AGC TGC CCC AGC CAG GCC CTG CAG CTG GCA GGC TGC TTG AGC ⁷⁶ 315
 Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
⁷⁷
 316 CAA CTC CAT AGC GGC CTT TTC CTC TAC CAG GGG CTC CTG CAG GCC ⁹¹ 360
 Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala
⁹²
 361 CTG GAA GGG ATC TCC CCC GAG TTG GGT CCC ACC TTG GAC ACA ¹⁰⁶ 405
 Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu
¹⁰⁷
 406 CAG CTG GAC GTC GCC GAC TTT GCC ACC ACC ATC TGG CAG CAG ¹²¹ 450
 Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met
¹²²
 451 GAA GAA CTG GGA ATG GCC CCT GCC CTG CAG CCC ACC CAG GGT GCC ¹³⁶ 495
 Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala
¹³⁷
 496 ATG CCG GCC TTC GCC TCT GCT TTC CAG CGC CGG GCA GGA GGG ¹⁵¹ 540
 Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val
¹⁵²
 541 CTA GTT GCC TCC CAT CTG CAG AGC TTC CTG GAG GTG TCG TAC CGC ¹⁶⁶ 585
 Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg
¹⁶⁷
 586 GTT CTA CGC CAC CTT GCC CAG CCC TAA TAA ¹⁷⁴ 616
 Val Leu Arg His Leu Ala Gln Pro stop codon

(see: SEQ ID NO: 18)

(see: SEQ ID NO: 19)

Fig. 4

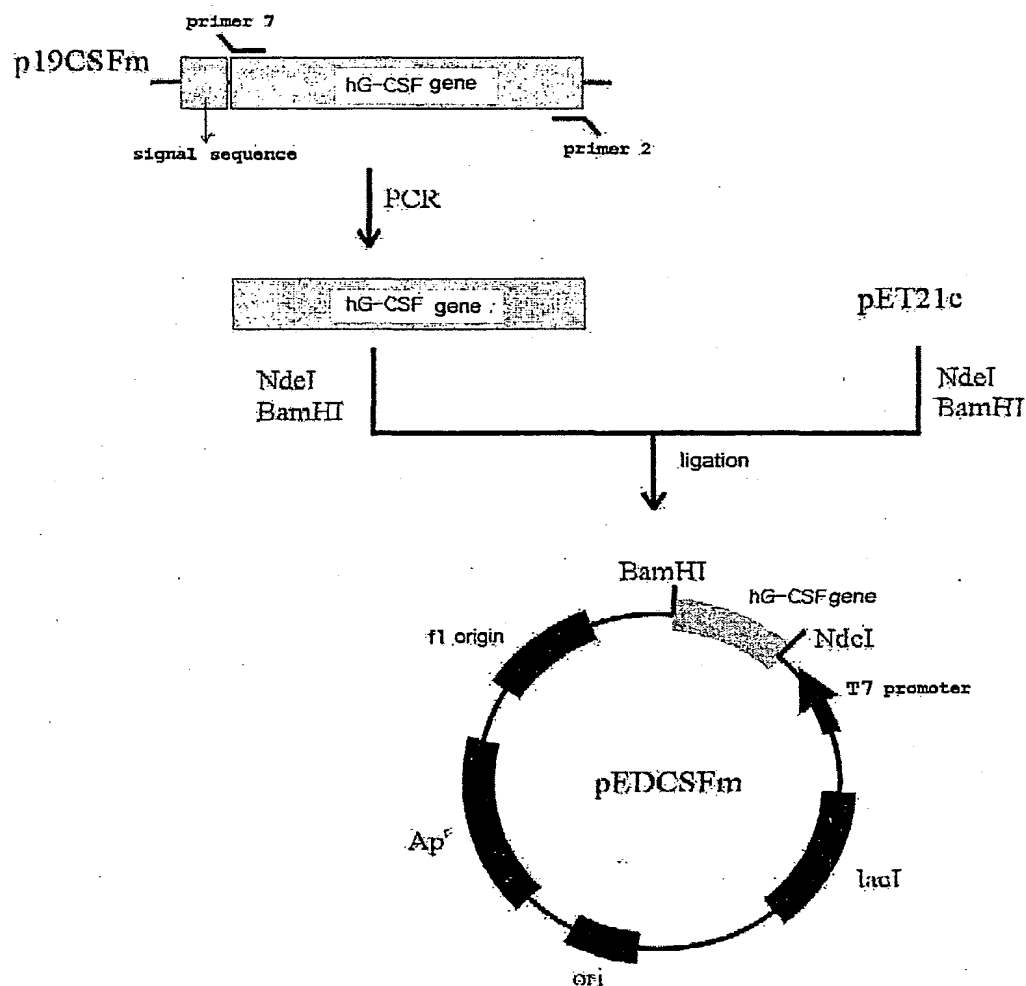


Fig. 5

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1      15
1 ATG ACC CCC CTG GGC CCT GCC AGC TCC CTG CCC CAG AGC TTC CTG 45
  Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu

16      30
46 CTC AAG TGC TTA GAG CAA GTG AGG AAG ATC CAG GGC GAT GGC GCA 90
  Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala

31      45
91 GCG CTC CAG GAG AAG CTG TGT GCC ACC TAC AAG CTG TGC CAC CCC 135
  Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro

46      60
136 GAG GAG CTG GTG CTG CTC GGA CAC TCT CTG GGC ATC CCC TGG GCT 180
  Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala

61      75
181 GCG CTG AGC AGC TGC CCC AGC CAG GCC CTG CAG CTG GCA GGC TGC 225
  Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys

76      90
226 TTG AGC CAA CTC CAT AGC GGC CTT TTC CTC TAC CAG GGG CTC CTG 270
  Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu

91      105
271 CAG GCC CTG GAA GGG ATC TCC CCC GAG TTG GGT CCC ACC TTG GAC 315
  Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp

106      120
316 ACA CTG CAG CTG GAC GTC GCC GAC TTT GCC ACC ACC ATC TGG CAG 360
  Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln

121      135
361 CAG ATG GAA GAA CTG GGA ATG GCC CCT GCC CTG CAG CCC ACC CAG 405
  Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln

136      150
406 GGT GCC ATG CCG GCC TTC GCC TCT GCT TTC CAG CGC CGG GCA GGA 450
  Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly

151      165
451 GGG GTC CTA GTT GCC TCC CAT CTG CAG AGC TTC CTG GAG GTG TCG 495
  Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser

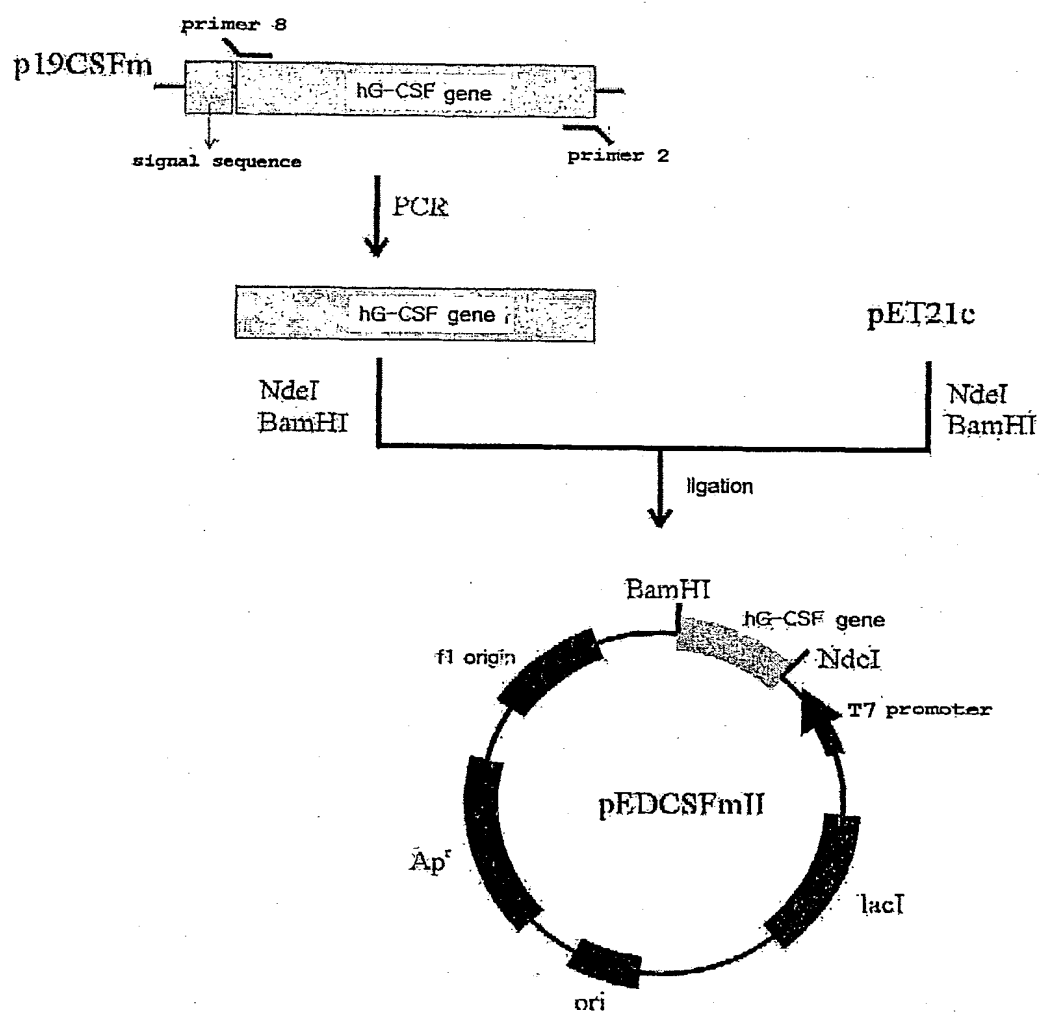
166      175
496 TAC CGC GTT CTA CGC CAC CTT GCC CAG CCC TAA TAA 531
  Tyr Arg Val Leu Arg His Leu Ala Gln Pro stop codon

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(see: SEQ ID NO: 20)

(see: SEQ ID NO: 21)

Fig. 6



1 15
1 ATG ACT CCG TTA GGT CCA GCC AGC TCC CTG CCC CAG AGC TTC CTG 45
Met. Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu
(see: SEQ ID NO: 22)
(see: SEQ ID NO: 23)

Fig. 8

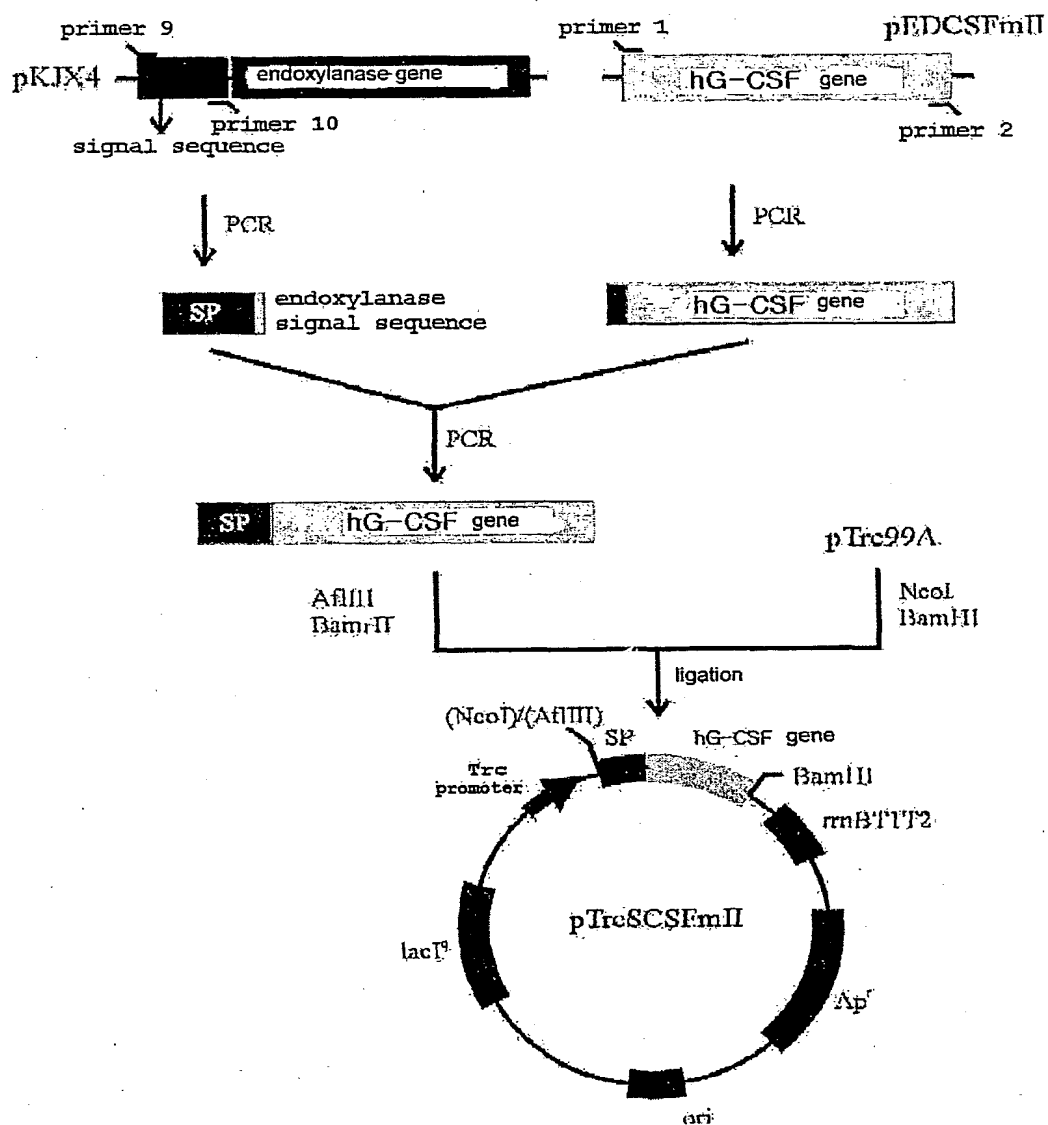


Fig. 9

-28 -14
 1 ATG TTT AAG TTT AAA AAG AAA TTC TTA GTG GGA TTA ACG GCA GCT 45
 Met Phe Lys Phe Lys Lys Lys Phe Leu Val Gly Leu Thr Ala Ala
 -13 -1 +1 2
 46 TTC ATG AGT ATC AGC ATG TTT TCT GCA ACC GCC TCT GCA ACT CCG 90
 Phe Met Ser Ile Ser Met Phe Ser Ala Thr Ala Ser Ala Thr Pro
 3 17
 91 TTA GGT CCA GCC AGC TCC CTG CCC CAG AGC TTC CTG CTC AAG TGC 135
 Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys

(see: SEQ ID NO: 24)

(see: SEQ ID NO: 25)

Fig. 10

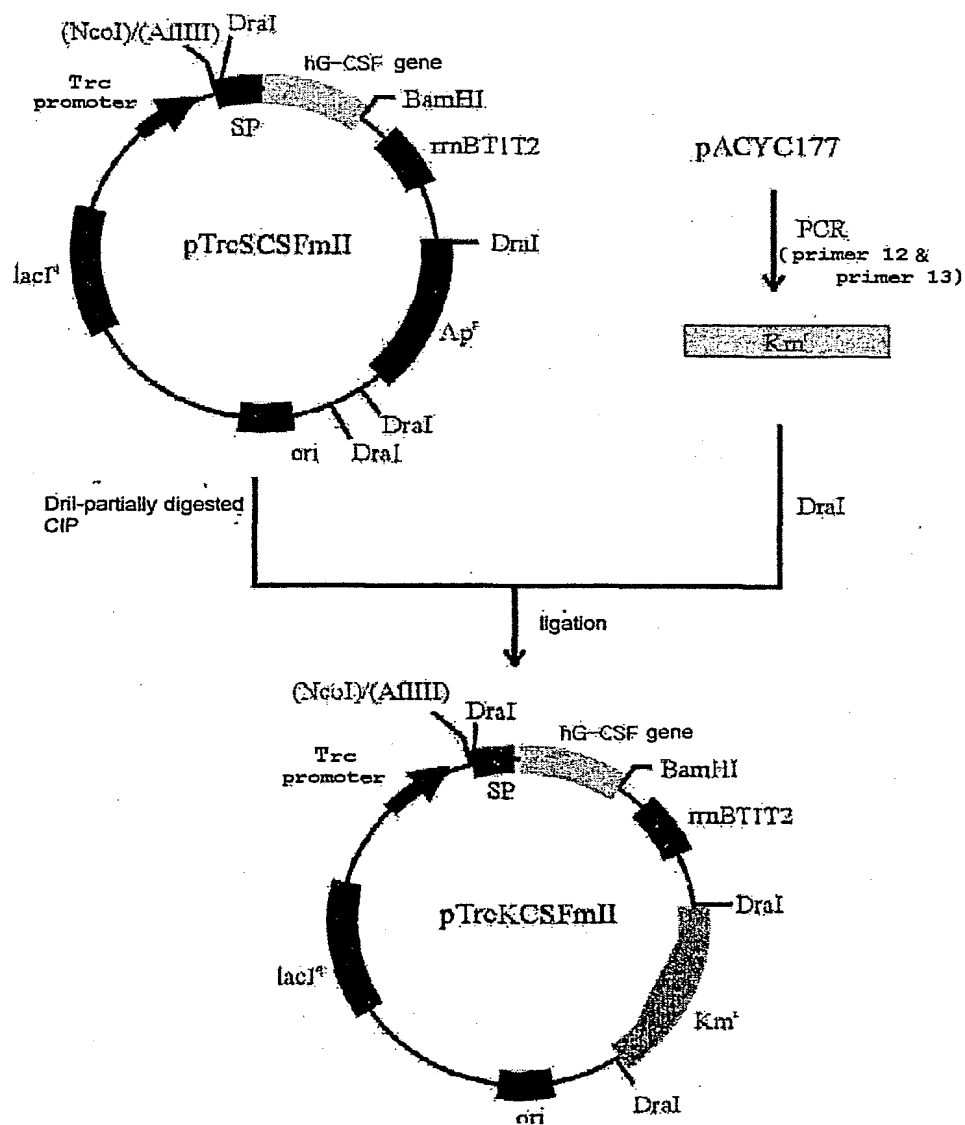


Fig. 11

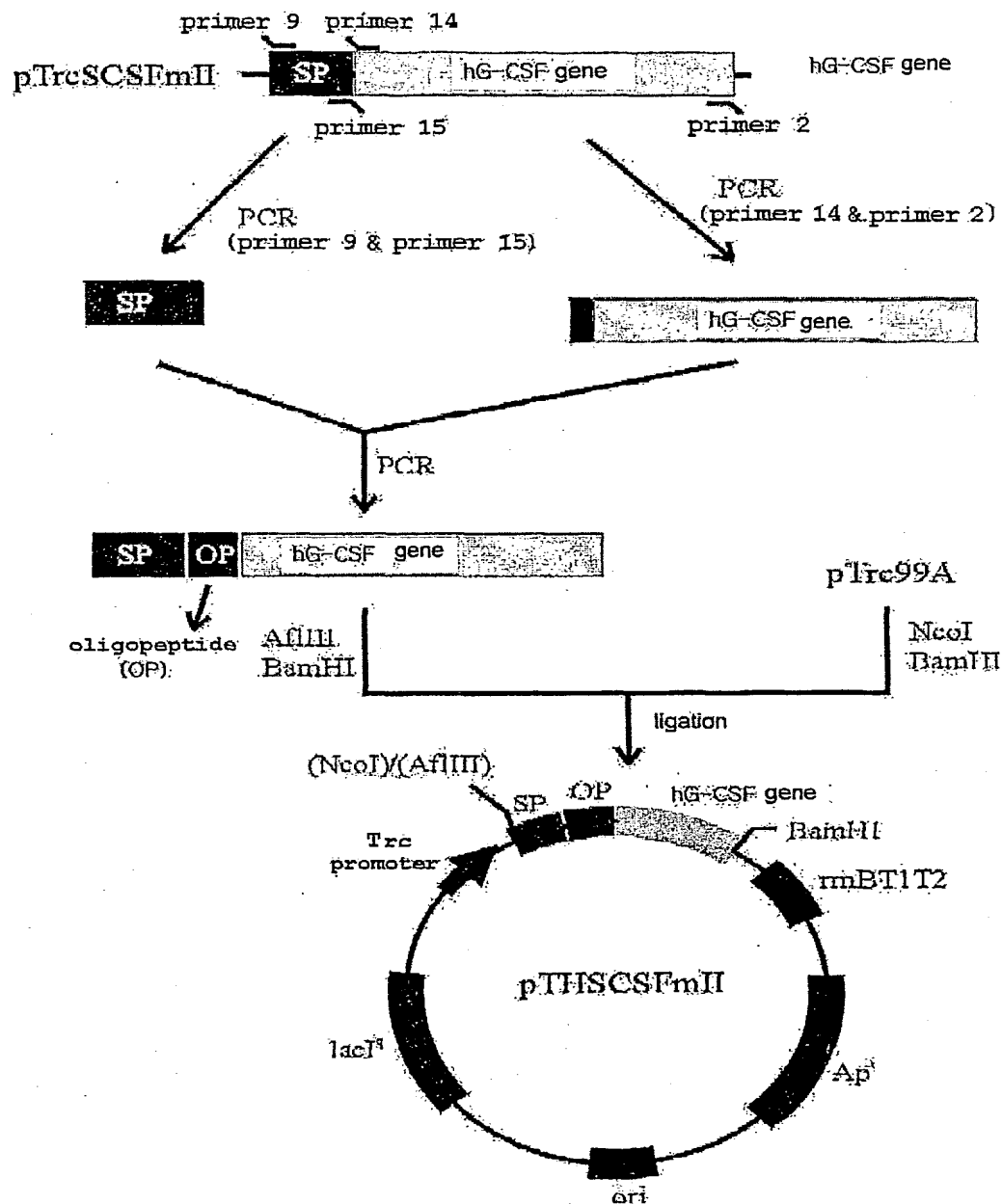


Fig. 12

-28 -14
1 ATG TTT AAG TTT AAA AAG AAA TTC TTA GTG GGA TTA ACG GCA GCT 45
Met Phe Lys Phe Lys Lys Lys Phe Leu Val Gly Leu Thr Ala Ala

-13 -1 +1 2
46 TTC ATG AGT ATC AGC ATG TTT TCT GCA ACC GCC TCT GCA GCT GGC 90
Phe Met Ser Ile Ser Met Phe Ser Ala Thr Ala Ser Ala Ala Gly

3 17
91 CCG CAC CAT CAC CAT CAC CAT ATC GAG GGA AGG ACT CCG TTA GGT 135
Pro His His His His His His Ile Glu Gly Arg Thr Pro Leu Gly

18 32
136 CCA GCC AGC TCC CTG CCC CAG AGC TTC CTG CTC AAG TGC TTA GAG 180
Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu Glu

(see: SEQ ID NO: 26)

(see: SEQ ID NO: 27)

Fig. 13

